SWISS-PROT: O60214

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ID   TRT2_HUMAN     STANDARD;      PRT;   297 AA.
AC   P45379; Q99596; Q99597; O60214;
DT   01-NOV-1995 (Rel. 32, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Troponin T, cardiac muscle isoforms (TnTC).
GN   TNNT2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 6).
RC   TISSUE=Heart;
RX   MEDLINE=93345675; PubMed=8344420; [NCBI, ExPASy, EBI, Israel, Japan]
RA   Mesnard L., Samson F., Espinasse I., Durand J., Neveux J.-Y.,
RA   Mercadier J.-J.;
RT   "Molecular cloning and developmental expression of human cardiac
RT   troponin T.";
RL   FEBS Lett. 328:139-144(1993).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 6).
RC   TISSUE=Heart muscle;
RX   MEDLINE=94375053; PubMed=8088824; [NCBI, ExPASy, EBI, Israel, Japan]
RA   Townsend P.J., Farza H., Macgeoch C., Spurr N.K., Wade R.,
RA   Gahlman R., Yacoub M.H., Barton P.J.R.;
RT   "Human cardiac troponin T: identification of fetal isoforms and
RT   assignment of the TNNT2 locus to chromosome 1q.";
RL   Genomics 21:311-316(1994).
RN   [3]
RP   SEQUENCE FROM N.A. (SPLICED ISOFORMS).
RC   TISSUE=Fetal heart;
RX   MEDLINE=96129582; PubMed=8576938; [NCBI, ExPASy, EBI, Israel, Japan]
RA   Townsend P.J., Barton P.J.R., Yacoub M.H., Farza H.;
RT   "Molecular cloning of human cardiac troponin T isoforms: expression in
RT   developing and failing heart.";
RL   J. Mol. Cell. Cardiol. 27:2223-2236(1995).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 6; 7 AND 8).
RC   TISSUE=Heart;
RX   MEDLINE=95202803; PubMed=7534662; [NCBI, ExPASy, EBI, Israel, Japan]
RA   Anderson P.A., Greig A., Mark T.M., Malouf N.N., Oakeley A.E.,
RA   Ungerleider R.M., Allen P.D., Kay B.K.;
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RT   the developing, adult, and failing heart.";
RL   Circ. Res. 76:681-686(1995).
RN   [5]
```

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6 AND 10).
RC TISSUE=Fetal heart;
RX MEDLINE=95202804; PubMed=7895342; [NCBI, ExPASy, EBI, Israel, Japan]
RA Mesnard L., Logeart D., Taviaux S., Diriong S., Mercadier J.-J.,
RA Samson F.;
RT "Human cardiac troponin T: cloning and expression of new isoforms in
RT the normal and failing heart.";
RL Circ. Res. 76:687-692(1995).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 6), AND VARIANT FHC ILE-119.
RC TISSUE=Heart muscle;
RX MEDLINE=98141687; PubMed=9482583; [NCBI, ExPASy, EBI, Israel, Japan]
RA Gerull B., Osterziel K.-J., Witt C., Dietz R., Thierfelder L.;
RT "A rapid protocol for cardiac troponin T gene mutation detection in
RT familial hypertrophic cardiomyopathy.";
RL Hum. Mutat. 11:179-182(1998).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 6).
RA D'Cruz L.G., Oberoi J., Mughal F., Steffensen U., Steffensen M.,
RA Kubo T., Mogensen J., McKoy G., O'Donnoghue A., Pondel M.,
RA McKenna W.J., Carter N.D., Baboonian C.;
RT "Genomic organization of the human cardiac troponin T gene (TNNT2) and
RT characterization of the candidate promoter region.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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RC TISSUE=Blood;
RA Farza H., Townsend P.J.;
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RN [9]
RP SEQUENCE OF 69-75 AND 176-181.
RC TISSUE=Heart;
RX MEDLINE=96007936; PubMed=7498159; [NCBI, ExPASy, EBI, Israel, Japan]
RA Kovalyov L.I., Shishkin S.S., Efimochkin A.S., Kovalyova M.A.,
RA Ershova E.S., Egorov T.A., Musalyamov A.K.;
RT "The major protein expression profile and two-dimensional protein
RT database of human heart.";
RL Electrophoresis 16:1160-1169(1995).
RN [10]
RP VARIANTS FHC ASN-88 AND GLN-101.
RX MEDLINE=94265260; PubMed=8205619; [NCBI, ExPASy, EBI, Israel, Japan]
RA Thierfelder L., Watkins H., Macrae C., Lamas R., McKenna W.,
RA Vosberg H.-P., Seidman J.G., Seidman C.E.;
RT "Alpha-tropomyosin and cardiac troponin T mutations cause familial
RT hypertrophic cardiomyopathy: a disease of the sarcomere.";
RL Cell 77:701-712(1994).
RN [11]
RP VARIANTS FHC.
RX MEDLINE=95206332; PubMed=7898523; [NCBI, ExPASy, EBI, Israel, Japan]
RA Watkins H., McKenna W.J., Thierfelder L., Suk H.J., Anan R.,
RA O'Donoghue A., Spirito P., Matsumori A., Moravec C.S., Seidman J.G.,
RA Seidman C.E.;
RT "Mutations in the genes for cardiac troponin T and alpha-tropomyosin
RT in hypertrophic cardiomyopathy.";
RL New Engl. J. Med. 332:1058-1064(1995).
RN [12]
RP VARIANT FHC PRO-287.
RA Erdmann J., Wischke S., Kallisch H., Riedel K., Heidenreich M.,
RA Fleck E., Regitz-Zagrosek V.;
RT "A novel missense Arg 278 Pro mutation in the troponin T gene

RT (TNNT2).";
RL Hum. Mutat. 12:364-364(1998).
RN [13]
RP VARIANT FHC LEU-103.
RX MEDLINE=99457222; PubMed=10525521; [NCBI, ExPASy, EBI, Israel, Japan]
RA Varnava A., Baboonian C., Davison F., de Cruz L., Elliott P.M.,
RA Davies M.J., McKenna W.J.;
RT "A new mutation of the cardiac troponin T gene causing familial
RT hypertrophic cardiomyopathy without left ventricular hypertrophy.";
RL Heart 82:621-624(1999).
CC -!- FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF
CC TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS
CC CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
CC -!- ALTERNATIVE PRODUCTS: At least 10 isoforms; isoform 1/TNT1 (shown
CC here), 2, 3, 4, 5, 6/TNT3, 7/TNT4, 8/TNT2, 9 and 10; may be
CC produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: Heart. The fetal heart shows a greater
CC expression in the atrium than in the ventricle, while the adult
CC heart shows a greater expression in the ventricle than in the
CC atrium. Isoform 6 predominates in normal adult heart. Isoforms 1,
CC 7 and 8 are expressed in fetal heart. Isoform 7 is also expressed
CC in failing adult heart.
CC -!- DISEASE: DEFECTS IN TNNT2 ARE ONE OF THE CAUSES OF FAMILIAL
CC HYPERTROPHIC CARDIOMYOPATHY (FHC) WHICH IS AN AUTOSOMAL DOMINANT
CC DISORDER CHARACTERIZED BY INCREASED MYOCARDIAL MASS WITH MYOCYTE
CC AND MYOFIBRILLAR DISARRAY. THIS FORM OF FHC IS KNOWN AS CMH2.
CC IT IS A DISEASE OF THE SARCOMERE.
CC -!- SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.
CC ----------

CC ----------
DR EMBL; S64668; AAB27731.1; ALT_SEQ. [EMBL / GenBank / DDBJ] [CoDingSequence]
DR EMBL; X74819; CAA52818.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
DR EMBL; L40162; AAA67422.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
DR EMBL; X79855; CAA56235.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
DR EMBL; X79856; CAA56236.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
DR EMBL; X79857; CAA56237.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
DR EMBL; X79858; CAA56238.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
DR EMBL; Y09626; CAA70839.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
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DR EMBL; Y09628; CAA70841.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
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DR EMBL; AF004409; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
DR EMBL; AF004410; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
DR EMBL; AF004411; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
DR EMBL; AF004412; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
DR EMBL; AF004413; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
DR EMBL; AF004414; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
DR EMBL; AF004415; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
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DR EMBL; AF004417; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
DR EMBL; AF004418; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
DR EMBL; AF004419; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
DR EMBL; AF004420; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]

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DR   EMBL; AF004421; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
DR   EMBL; AY044273; AAK92231.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
DR   EMBL; S71128; AAB30957.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
DR   EMBL; S71127; AAB30957.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
DR   Genew; HGNC:11949; TNNT2.
DR   MIM; 191045; -. [NCBI / EBI]
DR   GeneCards; TNNT2.
DR   GeneLynx; TNNT2.
DR   Ensembl; P45379. [Entry / Contig view]
DR   SOURCE; TNNT2.
DR   MIM; 115195; -. [NCBI / EBI]
DR   InterPro; IPR001978; Troponin.
DR   InterPro; Graphical view of domain structure.
DR   Pfam; PF00992; Troponin; 1.
DR   ProDom [Domain structure / List of seq. sharing at least 1 domain]
DR   BLOCKS; O60214.
DR   ProtoNet; O60214.
DR   ProtoMap; O60214.
DR   PRESAGE; P45379.
DR   DIP; P45379.
DR   ModBase; P45379.
DR   SWISS-2DPAGE; GET REGION ON 2D PAGE.
KW   Muscle protein; Alternative splicing; Multigene family;
KW   Phosphorylation; Disease mutation; Polymorphism; Cardiomyopathy.
FT   INIT_MET      0      0
FT   MOD_RES       1      1       PHOSPHORYLATION (BY CK2) (BY SIMILARITY).
FT   VARSPLIC     17     21       MISSING (IN ISOFORM 8).
FT   VARSPLIC     17     31       MISSING (IN ISOFORM 7).
FT   VARSPLIC     22     31       MISSING (IN ISOFORM 6).
FT   VARSPLIC     22     22       MISSING (IN ISOFORM 2 AND ISOFORM 4).
FT   VARSPLIC     53     53       MISSING (IN ISOFORM 3 AND ISOFORM 4).
FT   VARSPLIC     98    136       MISSING (IN ISOFORM 9).
FT   VARSPLIC    200    200       MISSING (IN ISOFORM 5).
FT   VARSPLIC    200    202       MISSING (IN ISOFORM 10).
FT   VARIANT      88     88       I -> N (IN FHC CMH2).
FT                                /FTId=VAR_007605.
FT   VARIANT     101    101       R -> Q (IN FHC CMH2).
FT                                /FTId=VAR_007606.
FT   VARIANT     103    103       R -> L (IN FHC CMH2).
FT                                /FTId=VAR_009194.
FT   VARIANT     119    119       F -> I (IN FHC CMH2).
FT                                /FTId=VAR_007607.
FT   VARIANT     138    138       R -> K.
FT                                /FTId=VAR_013021.
FT   VARIANT     169    169       MISSING (IN FHC CMH2).
FT                                /FTId=VAR_007608.
FT   VARIANT     172    172       E -> K (IN FHC CMH2).
FT                                /FTId=VAR_007609.
FT   VARIANT     248    248       S -> T.
FT                                /FTId=VAR_013022.
FT   VARIANT     253    253       E -> D (IN FHC CMH2).
FT                                /FTId=VAR_007610.
FT   VARIANT     262    262       K -> R.
FT                                /FTId=VAR_007611.
FT   VARIANT     287    287       R -> C (IN FHC CMH2).
FT                                /FTId=VAR_007612.
FT   VARIANT     287    287       R -> P (IN FHC CMH2).
FT                                /FTId=VAR_007613.
FT   CONFLICT    241    241       K -> E (IN REF. 8).
FT   CONFLICT    262    262       K -> R (IN REF. 8).
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SQ   SEQUENCE   297 AA;  35792 MW;  66FDCD1EE4A3C965 CRC64;
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     AKEAEDGPME ESKPKPRSFM PNLVPPKIPD GERVDFDDIH RKRMEKDLNE LQALIEAHFE
     NRKKEEEELV SLKDRIERRR AERAEQQRIR NEREKERQNR LAEERARREE EENRRKAEDE
     ARKKKALSNM MHFGGYIQKQ AQTERKSGKR QTEREKKKKI LAERRKVLAI DHLNEDQLRE
     KAKELWQSIY NLEAEKFDLQ EKFKQQKYEI NVLRNRINDN QKVSKTRGKA KVTGRWK
//
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P45379 in FASTA format
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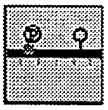
Direct BLAST submission at EMBnet-CH/SIB (Switzerland)


Direct BLAST submission at NCBI (Bethesda, USA)

ScanProsite, MotifScan

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)


Feature table viewer (Java)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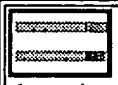
ProDom Release 2001.3 **Domain PD015088**	 Graphic representation of all proteins containing this domain.  Display the family as a tree. MSF Alignment in MSF format. Build an ESPript view  Run Predict Protein server with this domain 

Most frequent protein names	TRT2(7)
Commentary (automatic)	MUSCLE TROPONIN CARDIAC SKELETAL PHOSPHORYLATION ISOFORMS SPLICING ALTERNATIVE FAMILY
Alignment length	72
Number of domains in family	23
Consistency indicator	DIAMETER: 124 PAM RADIUS OF GYRATION: 38 PAM SEQUENCE CLOSEST TO CONSENSUS: TRT2_BOVIN 58-107 (distance:16 PAM)

ProDom Home Page **Query Form** **Blast Form** **References** **ProDom Complete Genomes**

Other descriptions of the family corresponding to this alignment 

	Sequence ID	start	end	weight	10 20 30 40 50
					---------|---------|---------|---------|---------|--
1	O13096_SALTR	42	104	4.27	.....EETPAEEASGETQDSKAKP-KSFMPNVAPPKLPEGDGKVDFDDLHR
5⊞	TRT1_HUMAN	.	.	2.27	.....REERPKPSRPVVPPLIPPKIPEGE-RVDFDDIHR
4⊞	TRT2_RAT	.	.	2.01	VEEVGPDEEAKDAEEGPVEDTKPKPSRLFMPNLVPPKIPDGE-RVDFDDIHR
8⊞	TRT2_HUMAN	.	.	4.25	.....EEGDREQEPGPGEESKPKPPRPFMPNLVPPKIPDGE-RVDFDDIHR
2⊞	O93376_SALSA	.	.	3.03	.....EQHFEEEKPK----FKPTAKAPKIPDGE-KVDFDDIQK
1	Q99L89_MOUSE	60	93	0.30	.....PKIPEGE-KVDFDDIQK
1	Q9QZ47_MOUSE	59	92	0.45	.....PKIPEGE-KVDFDDIQK
1	Q25148_HALRO	3	63	6.42	.....GEEEEPQQHHEDVEKP-MPRHSTTSIPRLPDGE-KVDLDVITQ
23	Consensus			23.00	VEEVGPEETGEEEEPGQHHEDKPKPSRPFMPNLAPPKIPDGEGKVDFDDIHR

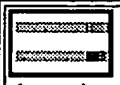
Minimal distance between sequences (in PAM)	20
Maximal number of clusters	12
If possible, clusterIDs should contain the following string (e.g.: human)	

To display a new alignment with these parameters, or click here to display all sequences in the family

Submit Query

Eukaryotic subfamily root	Bacterial subfamily root	Archaeal subfamily root	Viral subfamily root	Root of a subfamily that goes across domains of life

ProDom Home Page | Query Form | Blast Form | References | ProDom Complete Genomes

ProDom Release 2001.3 Domain PD349636	 Graphic representation of all proteins containing this domain.
	 Display the family as a tree.
	MSF Alignment in MSF format.
	Build an ESPript view 
	Run Predict Protein server with this domain 

Most frequent protein names	TRT2(6) TRT3(5)
Commentary (automatic)	MUSCLE TROPONIN SKELETAL PHOSPHORYLATION FAST MULTIGENE FAMILY ISOFORMS SPLICING
Alignment length	32
Number of domains in family	32
Consistency indicator	DIAMETER: 35 PAM RADIUS OF GYRATION: 14 PAM SEQUENCE CLOSEST TO CONSENSUS: Q9QUP7_MOUSE 88-117 (distance:7 PAM)

InterPro

ID	Accession number
"Troponin"	IPR001978

Pfam-A

ID	Accession number
Troponin	PF00992

ProDom Home Page | Query Form | Blast Form | References | ProDom Complete Genomes

Other descriptions of the family corresponding to this alignment 

	Sequence ID	start	end	weight	10 20 30
					---------|---------|---------|--
2	TRT2_CHICK	.	.	7.39	EHRKKEEEELISLKDRIEQRRAERAEQQRIRS
10	TRT2_HUMAN	.	.	6.60	ENRKKEEEELVSLKDRIEKRRAERAEQQRIRN
14	TRT3_RAT	.	.	5.54	EARKKEEEELVALKERIEKRRAERAEQQRIRA
1	Q9I8U9_BRARE	57	88	5.00	EHRQKEEEELIALRERIEKRRSERAEQQRIRT
5	TRT1_HUMAN	.	.	7.45	..RKKEEEELVALKDRIERRRSERAEQQRFRT
32	Consensus			31.98	EHRKKEEEELIALKDRIEKRRAERAEQQRIRT

Minimal distance between sequences (in PAM)	20
Maximal number of clusters	12
If possible, clusterIDs should contain the following string (e.g.: human)	

To display a new alignment with these parameters, or click here to display all sequences in the family

Submit Query

Eukaryotic subfamily root	Bacterial subfamily root	Archaeal subfamily root	Viral subfamily root	Root of a subfamily that goes across domains of life

ProDom Home Page | Query Form | Blast Form | References | ProDom Complete Genomes

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Printer-friendly view | Quick BlastP search

[General] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

General information about the entry

Entry name	**TRT2_HUMAN**
Primary accession number	**P45379**
Secondary accession numbers	Q99596 Q99597 O60214
Entered in SWISS-PROT in	Release 32, November 1995
Sequence was last modified in	Release 41, June 2002
Annotations were last modified in	Release 41, June 2002

Name and origin of the protein

Protein name	**Troponin T, cardiac muscle isoforms**
Synonym	**TnTC**
Gene name	**TNNT2**
From	Homo sapiens (Human) [TaxID: 9606]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

References

[1] SEQUENCE FROM NUCLEIC ACID (ISOFORM 6).
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MEDLINE=93345675; PubMed=8344420; [NCBI, ExPASy, EBI, Israel, Japan]
Mesnard L., Samson F., Espinasse I., Durand J., Neveux J.-Y., Mercadier J.-J.;
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MEDLINE=96129582; PubMed=8576938; [NCBI, ExPASy, EBI, Israel, Japan]
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MEDLINE=95202804; PubMed=7895342; [NCBI, ExPASy, EBI, Israel, Japan]
Mesnard L., Logeart D., Taviaux S., Diriong S., Mercadier J.-J., Samson F.;
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MEDLINE=98141687; PubMed=9482583; [NCBI, ExPASy, EBI, Israel, Japan]
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"Genomic organization of the human cardiac troponin T gene (TNNT2) and characterization of the candidate promoter region.";
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TISSUE=Blood;
Farza H., Townsend P.J.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

[9] SEQUENCE OF 69-75 AND 176-181.
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MEDLINE=96007936; PubMed=7498159; [NCBI, ExPASy, EBI, Israel, Japan]
Kovalyov L.I., Shishkin S.S., Efimochkin A.S., Kovalyova M.A., Ershova E.S., Egorov T.A., Musalyamov A.K.;
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Comments

- ***FUNCTION***: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
- ***ALTERNATIVE PRODUCTS***: At least 10 isoforms; isoform 1/TNT1 (shown here), 2, 3, 4, 5, 6/TNT3, 7/TNT4, 8/TNT2, 9 and 10; may be produced by alternative splicing.
- ***TISSUE SPECIFICITY***: Heart. The fetal heart shows a greater expression in the atrium than in the ventricle, while the adult heart shows a greater expression in the ventricle than in the atrium. Isoform 6 predominates in normal adult heart. Isoforms 1, 7 and 8 are expressed in fetal heart. Isoform 7 is also expressed in failing adult heart.
- ***DISEASE***: DEFECTS IN TNNT2 ARE ONE OF THE CAUSES OF FAMILIAL HYPERTROPHIC CARDIOMYOPATHY (FHC) WHICH IS AN AUTOSOMAL DOMINANT DISORDER CHARACTERIZED BY INCREASED MYOCARDIAL MASS WITH MYOCYTE AND MYOFIBRILLAR DISARRAY. THIS FORM OF FHC IS KNOWN AS CMH2. IT IS A DISEASE OF THE SARCOMERE.
- ***SIMILARITY***: BELONGS TO THE TROPONIN T FAMILY.

Copyright

Cross-references

S64668; AAB27731.1; ALT_SEQ.	[EMBL / GenBank / DDBJ] [CoDingSequence]
X74819; CAA52818.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
L40162; AAA67422.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
X79855; CAA56235.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
X79856; CAA56236.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
X79857; CAA56237.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
X79858; CAA56238.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
Y09626; CAA70839.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
Y09627; CAA70840.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
Y09628; CAA70841.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
AF004422; AAC39590.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]

EMBL	AF004409; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence] AF004410; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence] AF004411; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence] AF004412; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence] AF004413; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence] AF004414; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence] AF004415; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence] AF004416; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence] AF004417; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence] AF004418; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence] AF004419; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence] AF004420; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence] AF004421; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence] AY044273; AAK92231.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] S71128; AAB30957.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] S71127; AAB30957.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
Genew	HGNC:11949; TNNT2.
MIM	191045 [NCBI / EBI]. 115195 [NCBI / EBI].
GeneCards	TNNT2.
GeneLynx	TNNT2.
SOURCE	TNNT2; Homo sapiens.
Ensembl	P45379; Homo sapiens. [Entry / Contig view]
InterPro	IPR001978; Troponin. Graphical view of domain structure.
Pfam	PF00992; Troponin; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain].
BLOCKS	P45379.
ProtoNet	P45379.
ProtoMap	P45379.
PRESAGE	P45379.
DIP	P45379.
ModBase	P45379.
SWISS-2DPAGE	GET REGION ON 2D PAGE.

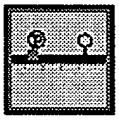
Keywords

Muscle protein; **Alternative splicing**; **Multigene family**; **Phosphorylation**; **Disease mutation**; **Polymorphism**; **Cardiomyopathy**.

Features

Key	From	To	Length	Description
INIT_MET	0	0		
MOD_RES	1	1		PHOSPHORYLATION (BY CK2) (*BY SIMILARITY*).
VARSPLIC	17	21		MISSING (IN ISOFORM 8).
VARSPLIC	17	31		MISSING (IN ISOFORM 7).
VARSPLIC	22	31		MISSING (IN ISOFORM 6).
VARSPLIC	22	22		MISSING (IN ISOFORM 2 AND ISOFORM 4).
VARSPLIC	53	53		MISSING (IN ISOFORM 3 AND

			ISOFORM 4).
VARSPLIC	98	136	MISSING (IN ISOFORM 9).
VARSPLIC	200	200	MISSING (IN ISOFORM 5).
VARSPLIC	200	202	MISSING (IN ISOFORM 10).
VARIANT	88	88	I -> N (IN FHC CMH2). /FTId=VAR_007605.
VARIANT	101	101	R -> Q (IN FHC CMH2). /FTId=VAR_007606.
VARIANT	103	103	R -> L (IN FHC CMH2). /FTId=VAR_009194.
VARIANT	119	119	F -> I (IN FHC CMH2). /FTId=VAR_007607.
VARIANT	138	138	R -> K. /FTId=VAR_013021.
VARIANT	169	169	MISSING (IN FHC CMH2). /FTId=VAR_007608.
VARIANT	172	172	E -> K (IN FHC CMH2). /FTId=VAR_007609.
VARIANT	248	248	S -> T. /FTId=VAR_013022.
VARIANT	253	253	E -> D (IN FHC CMH2). /FTId=VAR_007610.
VARIANT	262	262	K -> R. /FTId=VAR_007611.
VARIANT	287	287	R -> C (IN FHC CMH2). /FTId=VAR_007612.
VARIANT	287	287	R -> P (IN FHC CMH2). /FTId=VAR_007613.
CONFLICT	241	241	K -> E (IN REF. 8).
CONFLICT	262	262	K -> R (IN REF. 8).



Feature table viewer

Sequence information

Length: **297 AA** Molecular weight: **35792 Da** CRC64: **66FDCD1EE4A3C965** [This is a checksum on the sequence]

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        70         80         90        100        110        120
         |          |          |          |          |          |
AKEAEDGPME ESKPKPRSFM PNLVPPKIPD GERVDFDDIH RKRMEKDLNE LQALIEAHFE

       130        140        150        160        170        180
         |          |          |          |          |          |
NRKKEEEELV SLKDRIERRR AERAEQQRIR NEREKERQNR LAEERARREE EENRRKAEDE

       190        200        210        220        230        240
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ARKKKALSNM MHFGGYIQKQ AQTERKSGKR QTEREKKKKI LAERRKVLAI DHLNEDQLRE

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KAKELWQSIY NLEAEKFDLQ EKFKQQKYEI NVLRNRINDN QKVSKTRGKA KVTGRWK
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P45379 in FASTA format

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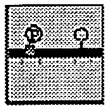
Direct BLAST submission at EMBnet-CH/SIB (Switzerland)


Direct BLAST submission at NCBI (Bethesda, USA)


ScanProsite, MotifScan


Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)


Feature table viewer (Java)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